1

## SEQUENCE LISTING

Merck Patent GmbH

<120> Glucose dehydrogenase fusion proteins and their
      use in expression systems

<130> 9906920-Bz-mi

<140>
<141>

<160> 16

<170> PatentIn Ver. 2.1

<210> 1
<211> 3992
<212> DNA
<213> Bacillus megaterium

<220>
<221> CDS
<222> (186)..(968)
<223> Glucose degydrogenase from Bacillus megaterum

<220>
<221> CDS
<222> (978)..(1010)
<223> Poly-histidine tag

<220>
<221> gene
<222> (1)..(3992)
<223> Plasmid PAW2

<400> 1
ccatcgaatg gccagatgat taattcctaa tttttgttga cactctatca ttgatagagt 60

tattttacca ctccctatca gtgatagaga aaagtgaaat gaatagttcg acaaaaatct 120

agataacgag ggcaatcgat gaattcgacc tcggtacccg gggatcccc gaggtcgacc 180

tgcag atg tat aca gat tta aaa gat aaa gta gtt gta att aca ggt gga 230
      Met Tyr Thr Asp Leu Lys Asp Lys Val Val Val Ile Thr Gly Gly
      1               5                   10                  15

tca aca ggt tta gga cgc gca atg gct gtt cgt ttc ggt caa gaa gaa 278
Ser Thr Gly Leu Gly Arg Ala Met Ala Val Arg Phe Gly Gln Glu Glu
                20                  25                  30

gca aaa gtt gtt att aac tat tac aac aat gaa gaa gaa gct cta gat 326
Ala Lys Val Val Ile Asn Tyr Tyr Asn Asn Glu Glu Glu Ala Leu Asp
                35                  40                  45

gcg aaa aaa gaa gta gaa gaa gca ggc gga caa gca atc atc gtt caa 374
Ala Lys Lys Glu Val Glu Glu Ala Gly Gly Gln Ala Ile Ile Val Gln
        50                  55                  60

```
ggc gat gta aca aaa gaa gaa gac gtt gta aat ctt gtt caa aca gct   422
Gly Asp Val Thr Lys Glu Glu Asp Val Val Asn Leu Val Gln Thr Ala
     65              70                  75

att aaa gaa ttt ggt aca tta gac gta atg att aac aac gct ggt gtt   470
Ile Lys Glu Phe Gly Thr Leu Asp Val Met Ile Asn Asn Ala Gly Val
 80              85                  90                  95

gaa aac cca gtt cct tct cat gag cta tct cta gat aac tgg aac aaa   518
Glu Asn Pro Val Pro Ser His Glu Leu Ser Leu Asp Asn Trp Asn Lys
                100                 105                 110

gtt att gat aca aac tta aca ggt gca ttc tta gga agc cgt gaa gca   566
Val Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala
             115                 120                 125

att aaa tac ttc gtt gaa aac gac att aaa gga aat gtt atc aac atg   614
Ile Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met
             130                 135                 140

tct agc gtt cac gaa atg att cct tgg cca tta ttt gtt cac tac gca   662
Ser Ser Val His Glu Met Ile Pro Trp Pro Leu Phe Val His Tyr Ala
             145                 150                 155

gca agt aaa ggc ggt atg aaa cta atg acg gaa aca ttg gct ctt gaa   710
Ala Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu
160                 165                 170                 175

tat gcg cca aaa ggt atc cgc gta aat aat att gga cca ggt gcg atg   758
Tyr Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Met
                180                 185                 190

aac aca cca att aac gca gag aaa ttt gca gat cca gaa caa cgt gca   806
Asn Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala
                195                 200                 205

gac gta gaa agc atg att cca atg ggt tac atc ggt aaa cca gaa gaa   854
Asp Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Lys Pro Glu Glu
             210                 215                 220

gta gca gca gtt gca gca ttc tta gct tca tca caa gca agc tat gta   902
Val Ala Ala Val Ala Ala Phe Leu Ala Ser Ser Gln Ala Ser Tyr Val
225                 230                 235

aca ggt att aca tta ttt gca gat ggc ggt atg acg aaa tac cct tct   950
Thr Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Lys Tyr Pro Ser
240                 245                 250                 255

ttc caa gca gga aga ggc taatagagc gct atg aga gga tcg cat cac cat  1001
Phe Gln Ala Gly Arg Gly         Ala Met Arg Gly Ser His His His
                260                         265

cac cat cac taatagaagc ttgacctgtg aagtgaaaaa tggcgcacat   1050
His His His
270

tgtgcgacat tttttttgtc tgccgtttac cgctactgcg tcacggatct ccacgcgccc  1110

tgtagcggcg cattaagcgc ggcgggtgtg gtggttacgc gcagcgtgac cgctacactt  1170
```

3

```
gccagcgccc tagcgcccgc tcctttcgct ttccttcctt cctttctcgc cacgttcgct 1230
ggcttttcccc gtcaagctct aaatcggggg ctccctttag ggttccgatt tagtgcttta 1290
cggcacctcg accccaaaaa acttgattag ggtgatggtt cacgtagtgg gccatcgccc 1350
tgatagacgg ttttttcgcc tttgacgttg gagtccacgt tctttaatag tggactcttg 1410
ttccaaactg gaacaacact caaccctatc tcggtctatt cttttgattt ataagggatt 1470
ttgccgattt cggcctattg gttaaaaaat gagctgattt aacaaaaatt taacgcgaat 1530
tttaacaaaa tattaacgct tacaattttca ggtggcactt ttcggggaaa tgtgcgcgga 1590
acccctattt gtttattttt ctaaatacat tcaaatatgt atccgctcat gagacaataa 1650
ccctgataaa tgcttcaata atattgaaaa aggaagagta tgagtattca acatttccgt 1710
gtcgccctta ttcccttttt tgcggcattt tgccttcctg ttttgctca cccagaaacg 1770
ctggtgaaag taaaagatgc tgaagatcag ttgggtgcac gagtgggtta catcgaactg 1830
gatctcaaca gcggtaagat ccttgagagt tttcgccccg aagaacgttt tccaatgatg 1890
agcacttttta aagttctgct atgtggcgcg gtattatccc gtattgacgc cgggcaagag 1950
caactcggtc gccgcataca ctattctcag aatgacttgg ttgagtactc accagtcaca 2010
gaaaagcatc ttacggatgg catgacagta agagaattat gcagtgctgc cataaccatg 2070
agtgataaca ctgcggccaa cttacttctg acaacgatcg gaggaccgaa ggagctaacc 2130
gcttttttgc acaacatggg ggatcatgta actcgccttg atcgttggga accggagctg 2190
aatgaagcca taccaaacga cgagcgtgac accacgatgc ctgtagcaat ggcaacaacg 2250
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attgatagac 2310
tggatggagg cggataaagt tgcaggacca cttctgcgct cggcccttcc ggctggctgg 2370
tttattgctg ataaatctgg agccggtgag cgtggctctc gcggtatcat tgcagcactg 2430
gggccagatg gtaagcccct ccgtatcgta gttatctaca cgacggggag tcaggcaact 2490
atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattggtag 2550
gaattaatga tgtctcgttt agataaaagt aaagtgatta acagcgcatt agagctgctt 2610
aatgaggtcg gaatcgaagg tttaacaacc cgtaaactcg cccagaagct aggtgtagag 2670
cagcctacat tgtattggca tgtaaaaaat aagcgggctt tgctcgacgc cttagccatt 2730
gagatgttag ataggcacca tactcacttt tgcctttag aagggaaag ctggcaagat 2790
tttttacgta ataacgctaa aagttttaga tgtgctttac taagtcatcg cgatggagca 2850
aaagtacatt taggtacacg gcctacagaa aaacagtatg aaactctcga aaatcaatta 2910
gcctttttat gccaacaagg ttttttcacta gagaatgcat tatatgcact cagcgcagtg 2970
```

4

```
ggcattttta ctttaggttg cgtattggaa gatcaagagc atcaagtcgc taaagaagaa 3030

agggaaacac ctactactga tagtatgccg ccattattac gacaagctat cgaattattt 3090

gatcaccaag gtgcagagcc agccttctta ttcggccttg aattgatcat atgcggatta 3150

gaaaacaac ttaaatgtga aagtgggtct taaaagcagc ataacctttt tccgtgatgg 3210

taacttcact agtttaaaag gatctaggtg aagatccttt ttgataatct catgaccaaa 3270

atcccttaac gtgagttttt gttccactga gcgtcagacc ccgtagaaaa gatcaaagga 3330

tcttcttgag atcctttttt tctgcgcgta atctgctgct tgcaaacaaa aaaaccaccg 3390

ctaccagcgg tggtttgttt gccggatcaa gagctaccaa ctcttttttcc gaaggtaact 3450

ggcttcagca gagcgcagat accaaatact gtccttctag tgtagccgta gttaggccac 3510

cacttcaaga actctgtagc accgcctaca tacctcgctc tgctaatcct gttaccagtg 3570

gctgctgcca gtggcgataa gtcgtgtctt accgggttgg actcaagacg atagttaccg 3630

gataaggcgc agcggtcggg ctgaacgggg ggttcgtgca cacagcccag cttggagcca 3690

acgacctaca ccgaactgag atacctacag cgtgagctat gagaaagcgc cacgcttcc 3750

gaagggagaa aggcggacag gtatccggta agcggcaggg tcggaacagg agagcgcacg 3810

agggagcttc cagggggaaa cgcctggtat ctttatagtc ctgtcgggtt tcgccacctc 3870

tgacttgagc gtcgattttt gtgatgctcg tcaggggggc ggagcctatg gaaaaacgcc 3930

agcaacgcgg cctttttacg gttcctggcc ttttgctggc cttttgctca catgaccga 3990

ca                                                                  3992
```

<210> 2
<211> 272
<212> PRT
<213> Bacillus megaterium (GlcDH-polytag fusion protein)

<400> 2

```
Met Tyr Thr Asp Leu Lys Asp Lys Val Val Val Ile Thr Gly Gly Ser
 1               5                  10                  15

Thr Gly Leu Gly Arg Ala Met Ala Val Arg Phe Gly Gln Glu Glu Ala
            20                  25                  30

Lys Val Val Ile Asn Tyr Tyr Asn Asn Glu Glu Glu Ala Leu Asp Ala
        35                  40                  45

Lys Lys Glu Val Glu Glu Ala Gly Gly Gln Ala Ile Ile Val Gln Gly
    50                  55                  60

Asp Val Thr Lys Glu Glu Asp Val Val Asn Leu Val Gln Thr Ala Ile
65                  70                  75                  80

Lys Glu Phe Gly Thr Leu Asp Val Met Ile Asn Asn Ala Gly Val Glu
            85                  90                  95
```

Asn Pro Val Pro Ser His Glu Leu Ser Leu Asp Asn Trp Asn Lys Val
            100                 105                 110

Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
            115                 120                 125

Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
            130                 135                 140

Ser Val His Glu Met Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                    165                 170                 175

Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Met Asn
            180                 185                 190

Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
            195                 200                 205

Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Lys Pro Glu Glu Val
            210                 215                 220

Ala Ala Val Ala Ala Phe Leu Ala Ser Ser Gln Ala Ser Tyr Val Thr
225                 230                 235                 240

Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Lys Tyr Pro Ser Phe
                    245                 250                 255

Gln Ala Gly Arg Gly Ala Met Arg Gly Ser His His His His His
            260                 265                 270


<210> 3
<211> 4193
<212> DNA
<213> Bacillus megaterium + Heamenteria ghilianii fusion gene

<220>
<221> gene
<222> (1)..(4193)
<223> Plasmid PAW4

<220>
<221> CDS
<222> (141)..(344)
<223> Tridegin

<220>
<221> CDS
<222> (387)..(1169)
<223> Glucose Dehydrogenase

<220>
<221> CDS
<222> (1179)..(1211)
<223> Poly-histidine tag

<400> 3

ccatcgaatg gccagatgat taattcctaa tttttgttga cactctatca ttgatagagt 60

tattttacca ctccctatca gtgatagaga aaagtgaaat gaatagttcg acaaaaatct 120

agataacgag ggcaatcgat atg aaa cta ttg cct tgc aaa gaa tgg cat caa 173
                        Met Lys Leu Leu Pro Cys Lys Glu Trp His Gln
                         1              5                      10

ggt att cct aac cct agg tgc tgg tgt ggg gct gat cta gaa tgc gca    221
Gly Ile Pro Asn Pro Arg Cys Trp Cys Gly Ala Asp Leu Glu Cys Ala
        15              20              25

caa gac caa tac tgt gcc ttc ata cct caa tgt aga cca aga tca gaa    269
Gln Asp Gln Tyr Cys Ala Phe Ile Pro Gln Cys Arg Pro Arg Ser Glu
        30              35              40

ctg att aaa cct atg gat gat ata tac caa aga cca gtc gag ttt cca    317
Leu Ile Lys Pro Met Asp Asp Ile Tyr Gln Arg Pro Val Glu Phe Pro
    45              50              55

aac ctt cca tta aaa cct agg gag gaa agcgctatga gaggatcgca          364
Asn Leu Pro Leu Lys Pro Arg Glu Glu
60              65

tcaccatcac catcacctgc ag atg tat aca gat tta aaa gat aaa gta gtt   416
                        Met Tyr Thr Asp Leu Lys Asp Lys Val Val
                            70                  75

gta att aca ggt gga tca aca ggt tta gga cgc gca atg gct gtt cgt    464
Val Ile Thr Gly Gly Ser Thr Gly Leu Gly Arg Ala Met Ala Val Arg
    80              35              90

ttc ggt caa gaa gaa gca aaa gtt gtt att aac tat tac aac aat gaa    512
Phe Gly Gln Glu Glu Ala Lys Val Val Ile Asn Tyr Tyr Asn Asn Glu
95              100             105             110

gaa gaa gct cta gat gcg aaa aaa gaa gta gaa gaa gca ggc gga caa    560
Glu Glu Ala Leu Asp Ala Lys Lys Glu Val Glu Glu Ala Gly Gly Gln
            115             120             125

gca atc atc gtt caa ggc gat gta aca aaa gaa gaa gac gtt gta aat    608
Ala Ile Ile Val Gln Gly Asp Val Thr Lys Glu Glu Asp Val Val Asn
        130             135             140

ctt gtt caa aca gct att aaa gaa ttt ggt aca tta gac gta atg att    656
Leu Val Gln Thr Ala Ile Lys Glu Phe Gly Thr Leu Asp Val Met Ile
    145             150             155

aac aac gct ggt gtt gaa aac cca gtt cct tct cat gag cta tct cta    704
Asn Asn Ala Gly Val Glu Asn Pro Val Pro Ser His Glu Leu Ser Leu
    160             165             170

gat aac tgg aac aaa gtt att gat aca aac tta aca ggt gca ttc tta    752
Asp Asn Trp Asn Lys Val Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu
175             180             185             190

gga agc cgt gaa gca att aaa tac ttc gtt gaa aac gac att aaa gga    800
Gly Ser Arg Glu Ala Ile Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly
            195             200             205

```
aat gtt atc aac atg tct agc gtt cac gaa atg att cct tgg cca tta   848
Asn Val Ile Asn Met Ser Ser Val His Glu Met Ile Pro Trp Pro Leu
        210             215             220

ttt gtt cac tac gca gca agt aaa ggc ggt atg aaa cta atg acg gaa   896
Phe Val His Tyr Ala Ala Ser Lys Gly Gly Met Lys Leu Met Thr Glu
        225             230             235

aca ttg gct ctt gaa tat gcg cca aaa ggt att cgc gta aat aat att   944
Thr Leu Ala Leu Glu Tyr Ala Pro Lys Gly Ile Arg Val Asn Asn Ile
240             245             250

gga cca ggt gcg atg aac aca cca att aac gca gag aaa ttt gca gat   992
Gly Pro Gly Ala Met Asn Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp
255             260             265             270

cca gaa caa cgt gca gac gta gaa agc atg att cca atg ggt tac atc  1040
Pro Glu Gln Arg Ala Asp Val Glu Ser Met Ile Pro Met Gly Tyr Ile
        275             280             285

ggt aaa cca gaa gaa gta gca gca gtt gca gca ttc tta gct tca tca  1088
Gly Lys Pro Glu Glu Val Ala Ala Val Ala Ala Phe Leu Ala Ser Ser
        290             295             300

caa gca agc tat gta aca ggt att aca tta ttt gca gat ggc ggt atg  1136
Gln Ala Ser Tyr Val Thr Gly Ile Thr Leu Phe Ala Asp Gly Gly Met
        305             310             315

acg aaa tac cct tct ttc caa gca gga aga ggc taatagagc gct atg aga 1187
Thr Lys Tyr Pro Ser Phe Gln Ala Gly Arg Gly         Ala Met Arg
320             325                             330

gga tcg cat cac cat cac cat cac taatagaagc ttgacctgtg aagtgaaaaa 1241
Gly Ser His His His His His His
        335             340

tggcgcacat tgtgcgacat tttttttgtc tgccgtttac cgctactgcg tcacggatct 1301

ccacgcgccc tgtagcggcg cattaagcgc ggcgggtgtg gtggttacgc gcagcgtgac 1361

cgctacactt gccagcgccc tagcgcccgc tcctttcgct ttcttccctt cctttctcgc 1421

cacgttcgcc ggctttcccc gtcaagctct aaatcggggg ctccctttag ggttccgatt 1481

tagtgcttta cggcacctcg accccaaaaa acttgattag ggtgatggtt cacgtagtgg 1541

gccatcgccc tgatagacgg ttttttcgccc tttgacgttg gagtccacgt tctttaatag 1601

tggactcttg ttccaaactg gaacaacact caaccctatc tcggtctatt cttttgattt 1661

ataagggatt ttgccgattt cggcctattg gttaaaaaat gagctgattt aacaaaaatt 1721

taacgcgaat tttaacaaaa tattaacgct tacaatttca ggtggcactt tcgggggaaa 1781

tgtgcgcgga acccctattt gtttattttt ctaaatacat tcaaatatgt atccgctcat 1841

gagacaataa ccctgataaa tgcttcaata atattgaaaa aggaagagta tgagtattca 1901

acatttccgt gtcgccctta ttcccttttt tgcggcattt tgccttcctg tttttgctca 1961
```

```
cccagaaacg ctggtgaaag taaaagatgc tgaagatcag ttgggtgcac gagtgggtta 2021

catcgaactg gatctcaaca gcggtaagat ccttgagagt tttcgccccg aagaacgttt 2081

tccaatgatg agcactttta aagttctgct atgtggcgcg gtattatccc gtattgacgc 2141

cgggcaagag caactcggtc gccgcataca ctattctcag aatgacttgg ttgagtactc 2201

accagtcaca gaaaagcatc ttacggatgg catgacagta agagaattat gcagtgctgc 2261

cataaccatg agtgataaca ctgcggccaa cttacttctg acaacgatcg gaggaccgaa 2321

ggagctaacc gcttttttgc acaacatggg ggatcatgta actcgccttg atcgttggga 2381

accggagctg aatgaagcca taccaaacga cgagcgtgac accacgatgc ctgtagcaat 2441

ggcaacaacg ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca 2501

attgatagac tggatggagg cggataaagt tgcaggacca cttctgcgct cggcccttcc 2561

ggctggctgg tttattgctg ataaatctgg agccggtgag cgtggctctc gcggtatcat 2621

tgcagcactg gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag 2681

tcaggcaact atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa 2741

gcattggtag gaattaatga tgtctcgttt agataaaagt aaagtgatta acagcgcatt 2801

agagctgctt aatgaggtcg gaatcgaagg tttaacaacc cgtaaactcg cccagaagct 2861

aggtgtagag cagcctacat tgtattggca tgtaaaaaat aagcgggctt tgctcgacgc 2921

cttagccatt gagatgttag ataggcacca tactcacttt tgccctttag aaggggaaag 2981

ctggcaagat tttttacgta ataacgctaa aagttttaga tgtgctttac taagtcatcg 3041

cgatggagca aaagtacatt taggtacacg gcctacagaa aaacagtatg aaactctcga 3101

aaatcaatta gcctttttat gccaacaagg tttttcacta gagaatgcat tatatgcact 3161

cagcgcagtg gggcatttta ctttaggttg cgtattggaa gatcaagagc atcaagtcgc 3221

taaagaagaa acggaaacac ctactactga tagtatgccg ccattattac gacaagctat 3281

cgaattattt gatcaccaag gtgcagagcc agccttctta ttggccttg aattgatcat 3341

atgcggatta gaaaaacaac ttaaatgtga aagtgggtct aaaagcagc ataacctttt 3401

tccgtgatgg taacttcact agtttaaaag gatctaggtg aagatccttt ttgataatct 3461

catgaccaaa atcccttaac gtgagttttc gttccactga gcgtcagacc ccgtagaaaa 3521

gatcaaagga tcttcttgag atccttttt tctgcgcgta atctgctgct tgcaaacaaa 3581

aaaaccaccg ctaccagcgg tggtttgttt gccggatcaa gagctaccaa ctcttttttcc 3641

gaaggtaact ggcttcagca gagcgcagat accaaatact gtccttctag tgtagccgta 3701

gttaggccac cacttcaaga actctgtagc accgcctaca tacctcgctc tgctaatcct 3761

gttaccagtg gctgctgcca gtggcgataa gtcgtgtctt accgggttgg actcaagacg 3821
```

atagttaccg gataaggcgc agcggtcggg ctgaacgggg ggttcgtgca cacagcccag 3881

cttggagcga acgacctaca ccgaactgag atacctacag cgtgagctat gagaaagcgc 3941

cacgcttccc gaagggagaa aggcggacag gtatccggta agcggcaggg tcggaacagg 4001

agagcgcacg agggagcttc caggggggaaa cgcctggtat ctttatagtc ctgtcgggtt 4061

tcgccacctc tgacttgagc gtcgattttt gtgatgctcg tcaggggggc ggagcctatg 4121

gaaaaacgcc agcaacgcgg cctttttacg gttcctggcc tttgctggc cttttgctca 4181

catgacccga ca                                                  4193


<210> 4
<211> 340
<212> PRT
<213> Bacillus megaterium + Heamenteria ghilianii fusion protein

<400> 4
Met Lys Leu Leu Pro Cys Lys Glu Trp His Gln Gly Ile Pro Asn Pro
 1               5                  10                  15

Arg Cys Trp Cys Gly Ala Asp Leu Glu Cys Ala Gln Asp Gln Tyr Cys
            20                  25                  30

Ala Phe Ile Pro Gln Cys Arg Pro Arg Ser Glu Leu Ile Lys Pro Met
        35                  40                  45

Asp Asp Ile Tyr Gln Arg Pro Val Glu Phe Pro Asn Leu Pro Leu Lys
    50                  55                  60

Pro Arg Glu Glu Met Tyr Thr Asp Leu Lys Asp Lys Val Val
65                  70                  75

Val Ile Thr Gly Gly Ser Thr Gly Leu Gly Arg Ala Met Ala Val Arg
        80                  85                  90

Phe Gly Gln Glu Glu Ala Lys Val Val Ile Asn Tyr Tyr Asn Asn Glu
    95                  100                 105                 110

Glu Glu Ala Leu Asp Ala Lys Lys Glu Val Glu Glu Ala Gly Gly Gln
            115                 120                 125

Ala Ile Ile Val Gln Gly Asp Val Thr Lys Glu Glu Asp Val Val Asn
            130                 135                 140

Leu Val Gln Thr Ala Ile Lys Glu Phe Gly Thr Leu Asp Val Met Ile
        145                 150                 155

Asn Asn Ala Gly Val Glu Asn Pro Val Pro Ser His Glu Leu Ser Leu
    160                 165                 170

Asp Asn Trp Asn Lys Val Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu
175                 180                 185                 190

Gly Ser Arg Glu Ala Ile Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly
            195                 200                 205

Asn Val Ile Asn Met Ser Ser Val His Glu Met Ile Pro Trp Pro Leu
210             215             220

Phe Val His Tyr Ala Ala Ser Lys Gly Gly Met Lys Leu Met Thr Glu
        225             230             235

Thr Leu Ala Leu Glu Tyr Ala Pro Lys Gly Ile Arg Val Asn Asn Ile
    240             245             250

Gly Pro Gly Ala Met Asn Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp
255             260             265             270

Pro Glu Gln Arg Ala Asp Val Glu Ser Met Ile Pro Met Gly Tyr Ile
            275             280             285

Gly Lys Pro Glu Glu Val Ala Ala Val Ala Ala Phe Leu Ala Ser Ser
        290             295             300

Gln Ala Ser Tyr Val Thr Gly Ile Thr Leu Phe Ala Asp Gly Gly Met
        305             310             315

Thr Lys Tyr Pro Ser Phe Gln Ala Gly Arg Gly Ala Met Arg Gly Ser
    320             325             330
His His His His His His
335             340

<210> 5
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<221> primer_bind
<222> (1)..(32)
<223> Primer 1, GlcDH

<220>
<223> Description of the artificial sequence: primer

<400> 5
gcgcgaattc atgtatacag atttaaaaag at                              32

<210> 6
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<221> primer_bind
<222> (1)..(31)
<223> Primer 2, GlcDH

<220>
<223> Description of the artificial sequence: primer

<400> 6
gcgcttcgaa ctattagcct cttcctgctt g                              31

<210> 7
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: primer

<400> 7
gcgcctgcag atgtatacag atttaaaaga t                           31


<210> 8
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<221> primer_bind
<222> (1)..(31)
<223> Primer 4, GlcDH

<220>
<223> Description of the artificial sequence: primer

<400> 8
gcgcagcgct ctattagcct cttcctgctt g                           31


<210> 9
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<221> primer_bind
<222> (1)..(31)
<223> Primer 5, Tridegin

<220>
<223> Description of the artificial sequence: primer

<400> 9
gcgcatcgat atgaaactat tgccttgcaa a                           31


<210> 10
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<221> primer_bind
<222> (1)..(31)
<223> Primer 6, Tridegin

<220>
<223> Description of the artificial sequence: primer

<400> 10
gcgcctgcag gtgatggtga tggtgatgcg a                                31


<210> 11
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<221> primer_bind
<222> (1)..(22)
<223> Primer 7, pASK 75UPN

<220>
<223> Description of the artificial sequence: primer

<400> 11
ccatcgaatg gccagatgat ta                                         22


<210> 12
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<221> primer_bind
<222> (1)..(21)
<223> pASK 75 RPN

<220>
<223> Description of the artificial sequence: primer

<400> 12
tagcggtaaa cggcagacaa a                                          21


<210> 13
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<221> primer_bind
<222> (1)..(20)
<223> Primer 9, T7 Seq.

<220>
<223> Description of the artificial sequence: primer

<400> 13
taatacgact cactataggg                                            20


<210> 14
<211> 18
<212> DNA
<213> Artificial sequence

<220>

13

<221> primer_bind
<222> (1)..(18)
<223> Rev. Seq.

<220>
<223> Description of the artificial sequence: primer

<400> 14
tagaaggcac agtcgagg                                          18